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SEQUENCE LISTING

<110> MIYATA, Toshio

<120> A Method for Detecting Megsin Protein and Use
Thereof

<130> SHIM-012

<140> 09/936,883

<141> 2001-12-21

<150> JP 1999-75305

<151> 1999-03-19

<150> JP 1999-306623

<151> 1999-10-28

<160> 21

<170> PatentIn Ver. 2.0

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(1140)

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<302> A mesangium-predominant gene, megsin, is a new serpin
upregulated in IgA nephropathy.

<303> J. Clin. Invest.

<304> 120

<305> 4

<306> 828-836

<307> 1998-08-15

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Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
20 25 30

ctg agc ctc ttc gct gcc ctg gcc gtc cgc ttg ggc gct caa gat 144
Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp
35 40 45

gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca 192
Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
50 55 60

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gga tat gga aac tct tct aat agt cag tca ggg ctc cag tct caa ctg	240
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65 70 75 80	
aaa aga gtt ttt tct gat ata aat gca tcc cac aag gat tat gat ctc	288
Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu	
85 90 95	
agc att gtg aat ggg ctt ttt gct gaa aaa gtg tat ggc ttt cat aag	336
Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys	
100 105 110	
gac tac att gag tgt gcc gaa aaa tta tac gat gcc aaa gtg gag cga	384
Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg	
115 120 125	
gtt gac ttt acg aat cat tta gaa gac act aga cgt aat att aat aag	432
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130 135 140	
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Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu	
145 150 155 160	
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Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met	
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Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu	
225 230 235 240	
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245 250 255	
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Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys	
275 280 285	
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act gct gcc aca gga agt aat att gta gaa aag caa ctc cct cag tcc															1056	
Thr	Ala	Ala	Thr	Gly	Ser	Asn	Ile	Val	Glu	Lys	Gln	Leu	Pro	Gln	Ser	
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Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp																
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Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser																
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Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu																
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Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu																
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Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys																
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Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg																
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Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys																
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Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
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Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
165 170 175

Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
180 185 190

Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
195 200 205

His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
210 215 220

Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
225 230 235 240

Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
245 250 255

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
260 265 270

Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys
275 280 285

Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys
290 295 300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
305 310 315 320

Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala
325 330 335

Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser
340 345 350

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<211> 15

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<211> 16

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

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<310> PCT/JP98/04269
<311> 1998-09-22

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Leu	Phe	Arg	Glu	Met	Asp	Ser	Ser	Gln	Gly	Asn	Gly	Asn	Val	Phe	Phe	
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tct tcc ctg agc atc ttc act gcc ctg agc cta atc cgt ttg ggt gct															145	
Ser	Ser	Leu	Ser	Ile	Phe	Thr	Ala	Leu	Ser	Leu	Ile	Arg	Leu	Gly	Ala	
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Arg	Gly	Asp	Cys	Xaa	Arg	Gln	Ile	Asp	Lys	Ala	Leu	His	Phe	Ile	Ser	
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cca tca aga caa ggg aat tca tcg aac agt cag cta gga ctg caa tat															241	
Pro	Ser	Arg	Gln	Gly	Asn	Ser	Ser	Asn	Ser	Gln	Leu	Gly	Leu	Gln	Tyr	
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caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag gat nnn															289	
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35 40 45

Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser
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Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu
85 90 95

Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys
100 105 110

Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg
115 120 125

Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys
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Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp
145 150 155 160

Ser Ser Leu Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
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Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser
180 185 190

Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met
195 200 205

His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met
210 215 220

Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met
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Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln
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Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val
260 265 270

Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg
275 280 285

Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg
290 295 300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys
305 310 315 320

Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala
325 330 335

Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser

340

345

350

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<210> 20
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 20 25 30

ggg gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt 144
 Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
 35 40 45

aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt 192
 Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu
 50 55 60

cag tat caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag 240
 Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys
 65 70 75 80

gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat 288
 Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr
 85 90 95

gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct 336
 Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala
 100 105 110

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 115 120 125

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145	150	155	160
aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act			528
Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr			
165	170	175	
gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta			576
Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val			
180	185	190	
gtt aat atg atg cat caa gaa cgg cgg ttc aat ttg tct acc att cag			624
Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln			
195	200	205	
cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc			672
Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser			
210	215	220	
atg tac att atg ctg cct gag gat ggc cta tgt gaa att gaa agc aag			720
Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys			
225	230	235	240
ctg agt ttc cag aat ctg atg gac tgg acc aat agg agg aaa atg aaa			768
Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys			
245	250	255	
tct cag tat gtg aac gtg ttt ctc ccc cag ttc aag ata gag aag aat			816
Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn			
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Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe			
275	280	285	
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Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu			
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tac gta tca aag cta atg cac aag tca ttc ata gag gtc tca gag gag			960
Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu			
305	310	315	320
ggc act gaa gcc act gct gcc aca gaa aat aac att gtt gaa aag cag			1008
Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln			
325	330	335	
ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc			1056
Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val			
340	345	350	
atc aag aag aat gac atc atc tta ttt act ggc aaa gtc tct tgt cct			1104
Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro			
355	360	365	

tgaattcga tttggtttcc tatacagtaa caggcatcaa gaa

1147

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Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu
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Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
35 40 45
Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu
50 55 60
Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys
65 70 75 80
Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr
85 90 95
Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala
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Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe
115 120 125
Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys
130 135 140
Val Leu Gly Asp Ser Ser Leu Ser Ser Ala Val Met Val Leu Val
145 150 155 160
Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr
165 170 175
Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val
180 185 190
Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln
195 200 205
Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser
210 215 220
Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys
225 230 235 240
Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys
245 250 255

Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn
260 265 270

Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe
275 280 285

Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu
290 295 300

Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu
305 310 315 320

Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln
325 330 335

Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val
340 345 350

Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro
355 360 365